

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/625, 115A

Source: FW16

Date Processed by STIC: 8/15/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/15/2005

PATENT APPLICATION: US/10/625,115A

TIME: 11:49:59

Input Set : A:\Sequence.ST25.txt

Output Set: N:\CRF4\08152005\J625115A.raw

3 <110> APPLICANT: Nielsen, Bjarne R.
 4 Nielsen, Ruby
 5 Lehmbeck, Jan
 7 <120> TITLE OF INVENTION: Thermostable Glucoamylase
 9 <130> FILE REFERENCE: 5279.210-US
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/625,115A
 C--> 11 <141> CURRENT FILING DATE: 2003-07-22
 11 <160> NUMBER OF SEQ ID NOS: 35
 13 <170> SOFTWARE: PatentIn version 3.3
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 25
 17 <212> TYPE: PRT
 18 <213> ORGANISM: Talaromyces emersonii
 21 <220> FEATURE:
 22 <221> NAME/KEY: misc_feature
 23 <223> OTHER INFORMATION: Xaa at position 13 denotes a residue that could
 24 not be assigned
 26 <400> SEQUENCE: 1
 W--> 28 Ala Asn Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Xaa Pro Ile Ala
 29 1 5 10 15
 32 Leu Gln Gly Val Leu Asn Asn Ile Gly
 33 20 25
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 20
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Talaromyces emersonii
 41 <400> SEQUENCE: 2
 43 Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser Thr Gly Gly Leu
 44 1 5 10 15
 47 Gly Glu Pro Lys
 48 20
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 22
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Talaromyces emersonii
 57 <220> FEATURE:
 58 <221> NAME/KEY: misc_feature
 59 <222> LOCATION: (0)..(22)
 60 <223> OTHER INFORMATION: Xaa denotes a residue that could not be assigned
 62 <400> SEQUENCE: 3
 W--> 64 Xaa Asn Val Asn Glu Thr Ala Phe Thr Gly Pro Xaa Gly Arg Pro Gln
 65 1 5 10 15
 68 Arg Asp Gly Pro Ala Leu

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69          20
72 <210> SEQ ID NO: 4
73 <211> LENGTH: 35
74 <212> TYPE: PRT
75 <213> ORGANISM: Talaromyces emersonii
77 <400> SEQUENCE: 4
79 Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly
80 1          5          10          15
83 Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala
84          20          25          30
87 Asn His Lys
88          35
91 <210> SEQ ID NO: 5
92 <211> LENGTH: 16
93 <212> TYPE: PRT
94 <213> ORGANISM: Talaromyces emersonii
97 <220> FEATURE:
98 <221> NAME/KEY: misc_feature
99 <222> LOCATION: (0)..(16)
100 <223> OTHER INFORMATION: Xaa denotes a residue that could not be assigned
102 <400> SEQUENCE: 5
W--> 104 Thr Xaa Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys
105 1          5          10          15
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 35
110 <212> TYPE: PRT
111 <213> ORGANISM: Talaromyces emersonii
113 <400> SEQUENCE: 6
115 Ala Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
116 1          5          10          15
119 Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu Asp Asp
120          20          25          30
123 Ser Trp Gln
124          35
127 <210> SEQ ID NO: 7
128 <211> LENGTH: 591
129 <212> TYPE: PRT
130 <213> ORGANISM: Talaromyces emersonii
132 <400> SEQUENCE: 7
134 Ala Thr Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala
135 1          5          10          15
138 Leu Gln Gly Val Leu Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala
139          20          25          30
142 Gly Ala Ser Ala Gly Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro
143          35          40          45
146 Asn Tyr Phe Tyr Ser Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr
147          50          55          60
150 Leu Val Asp Ala Phe Asn Arg Gly Asn Lys Asp Leu Glu Gln Thr Ile
151 65          70          75          80

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```

154 Gln Gln Tyr Ile Ser Ala Gln Ala Lys Val Gln Thr Ile Ser Asn Pro
155      85      90      95
158 Ser Gly Asp Leu Ser Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn Val
159      100     105     110
162 Asn Glu Thr Ala Phe Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly
163      115     120     125
166 Pro Ala Leu Arg Ala Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile
167      130     135     140
170 Asp Asn Gly Glu Ala Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val
171 145      150     155     160
174 Gln Asn Asp Leu Ser Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe
175      165     170     175
178 Asp Leu Trp Glu Glu Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val
179      180     185     190
182 Gln His Arg Ala Leu Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn
183      195     200     205
186 His Thr Cys Ser Asn Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe
187      210     215     220
190 Leu Gln Ser Tyr Trp Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly
191 225      230     235     240
194 Ser Gly Arg Ser Gly Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His
195      245     250     255
198 Thr Phe Asp Pro Ala Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys
199      260     265     270
202 Ser Ala Arg Ala Leu Ala Asn His Lys Val Val Thr Asp Ser Phe Arg
203      275     280     285
206 Ser Ile Tyr Ala Ile Asn Ser Gly Ile Ala Glu Gly Ser Ala Val Ala
207      290     295     300
210 Val Gly Arg Tyr Pro Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr
211 305      310     315     320
214 Leu Ala Thr Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln
215      325     330     335
218 Trp Lys Lys Ile Gly Ser Ile Ser Ile Thr Asp Val Ser Leu Pro Phe
219      340     345     350
222 Phe Gln Asp Ile Tyr Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly
223      355     360     365
226 Ser Thr Thr Phe Asn Asp Ile Ile Ser Ala Val Gln Thr Tyr Gly Asp
227      370     375     380
230 Gly Tyr Leu Ser Ile Val Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu
231 385      390     395     400
234 Thr Glu Gln Phe Ser Arg Thr Asp Gly Thr Pro Leu Ser Ala Ser Ala
235      405     410     415
238 Leu Thr Trp Ser Tyr Ala Ser Leu Leu Thr Ala Ser Ala Arg Arg Gln
239      420     425     430
242 Ser Val Val Pro Ala Ser Trp Gly Glu Ser Ser Ala Ser Ser Val Leu
243      435     440     445
246 Ala Val Cys Ser Ala Thr Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr
247      450     455     460
250 Asn Thr Val Trp Pro Ser Ser Gly Ser Gly Ser Ser Thr Thr Thr Ser

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```

251 465          470          475          480
254 Ser Ala Pro Cys Thr Thr Pro Thr Ser Val Ala Val Thr Phe Asp Glu
255          485          490          495
258 Ile Val Ser Thr Ser Tyr Gly Glu Thr Ile Tyr Leu Ala Gly Ser Ile
259          500          505          510
262 Pro Glu Leu Gly Asn Trp Ser Thr Ala Ser Ala Ile Pro Leu Arg Ala
263          515          520          525
266 Asp Ala Tyr Thr Asn Ser Asn Pro Leu Trp Tyr Val Thr Val Asn Leu
267          530          535          540
270 Pro Pro Gly Thr Ser Phe Glu Tyr Lys Phe Phe Lys Asn Gln Thr Asp
271 545          550          555          560
274 Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro
275          565          570          575
278 Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu Asp Asp Ser Trp Gln
279          580          585          590
282 <210> SEQ ID NO: 8
283 <211> LENGTH: 1605
284 <212> TYPE: DNA
285 <213> ORGANISM: Aspergillus niger
288 <220> FEATURE:
289 <221> NAME/KEY: CDS
290 <222> LOCATION: (1)..(1602)
292 <220> FEATURE:
293 <221> NAME/KEY: sig_peptide
294 <222> LOCATION: (1)..(72)
296 <220> FEATURE:
297 <221> NAME/KEY: mat_peptide
298 <222> LOCATION: (73)..()
300 <400> SEQUENCE: 8
301 atg tcg ttc cga tct cta ctc gcc ctg agc ggc ctc gtc tgc aca ggg      48
302 Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
303          -20          -15          -10
305 ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc      96
306 Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
307          -5          -1 1          5
309 aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg      144
310 Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
311 10          15          20
313 gac ggt gct tgg gtg tcg ggc gcg gac tct ggc att gtc gtt gct agt      192
314 Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
315 25          30          35          40
317 ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct      240
318 Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
319          45          50          55
321 ggt ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc      288
322 Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
323          60          65          70
325 agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc      336
326 Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val

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327	75	80	85	
329	cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc	384		
330	Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu			
331	90 95 100			
333	ggt gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg	432		
334	Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp			
335	105 110 115 120			
337	gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc	480		
338	Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile			
339	125 130 135			
341	ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg	528		
342	Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr			
343	140 145 150			
345	gac att gtt tgg ccc ctc gtt agg aac gac ctg tcg tat gtg gct caa	576		
346	Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln			
347	155 160 165			
349	tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tcg	624		
350	Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Val Asn Gly Ser			
351	170 175 180			
353	tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt	672		
354	Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser			
355	185 190 195 200			
357	gcc ttc gcg acg gcc gtc ggc tcg tcc tgc tcc tgg tgt gat tct cag	720		
358	Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln			
359	205 210 215			
361	gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc	768		
362	Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe			
363	220 225 230			
365	att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc	816		
366	Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr			
367	235 240 245			
369	ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac	864		
370	Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp			
371	250 255 260			
373	tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag	912		
374	Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu			
375	265 270 275 280			
377	gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt	960		
378	Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser			
379	285 290 295			
381	gac agc gag gct gtt gcg gtg ggt ccg tac cct gag gac acg tac tac	1008		
382	Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr			
383	300 305 310			
385	aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg	1056		
386	Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu			
387	315 320 325			
389	tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca	1104		
390	Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr			
391	330 335 340			

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/625,115A

DATE: 08/15/2005
TIME: 11:50:00

Input Set : A:\Sequence.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 13
Seq#:3; Xaa Pos. 1,12
Seq#:5; Xaa Pos. 2
Seq#:11; N Pos. 3
Seq#:12; N Pos. 3,6
Seq#:13; N Pos. 6
Seq#:15; N Pos. 15

VERIFICATION SUMMARY

DATE: 08/15/2005

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TIME: 11:50:00

Input Set : A:\Sequence.ST25.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:743 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:760 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:777 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:806 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:15
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0